RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/619,310

DATE: 11/05/2001
TIME: 13:21:01

Input Set : A:\2001-09-28 seqlist.ST25.txt
Output Set: N:\CRF3\11022001\I619310.raw

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 5 <110> APPLICANT: BioImage A/S
 7         Thastrup, Ole
11 <120> TITLE OF INVENTION: Novel Florescent Proteins
15 <130> FILE REFERENCE: 3759-0106P
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/619,310
C--> 21 <141> CURRENT FILING DATE: 2000-07-19
25 <160> NUMBER OF SEQ ID NOS: 8
29 <170> SOFTWARE: PatentIn version 3.1
33 <210> SEQ ID NO: 1
35 <211> LENGTH: 764
37 <212> TYPE: DNA
39 <213> ORGANISM: Aequorea victoria
43 <220> FEATURE:
45 <221> NAME/KEY: CDS
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58 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt       97
59 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
60 15              20                  25                  30
62 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt      145
63 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
64              35                  40                  45
66 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act      193
67 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
68          50                  55                  60
70 act ttc tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg      241
71 Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
72          65                  70                  75
74 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag      289
75 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
76      80                  85                  90
78 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct      337
79 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
80 95                  100                 105                 110
82 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa      385
83 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
84              115                 120                 125
86 ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa      433
87 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
88              130                 135                 140
90 tac aac tat aac tca cat aat gta tac atc atg gca gac aaa cca aag      481
91 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
92          145                 150                 155
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94 aat gga atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga        529
95 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
96       160                   165                 170
98 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat     .  577
99 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
100 175                 180                 185                 190
102 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc       625
103 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
104                 195                 200                 205
106 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag       673
107 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
108             210                 215                 220
110 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa       721
111 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
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121 <212> TYPE: PRT
123 <213> ORGANISM: Aequorea victoria
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134             20                  25                  30
137 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
138             35                  40                  45
141 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
142       50                  55                  60
145 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
146 65                  70                  75                  80
149 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
150                 85                  90                  95
153 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
154                 100                 105                 110
157 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
158             115                 120                 125
161 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
162       130                 135                 140
165 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
166 145                 150                 155                 160
169 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
170                 165                 170                 175
173 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
174             180                 185                 190
177 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
178             195                 200                 205
181 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
182             210                 215                 220
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 201 <221> NAME/KEY: CDS
 203 <222> LOCATION: (1)..(717)
 205 <223> OTHER INFORMATION:
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 212 1               5                   10                  15
 214 gaa tta gat ggc gat gtt aat ggg caa aaa ttc tcc gtt agt gga gag       96
 215 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
 216             20                  25                  30
 218 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc      144
 219 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 220         35                  40                  45
 222 act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc      192
 223 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 224     50                  55                  60
 226 tct cat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag      240
 227 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 228 65              70                  75                  80
 230 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga      288
 231 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 232             85                  90                  95
 234 act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc      336
 235 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 236             100                 105                 110
 238 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att      384
 239 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 240         115                 120                 125
 242 gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat      432
 243 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
 244     130                 135                 140
 246 tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc      480
 247 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
 248 145                 150                 155                 160
 250 atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga agc gtt      528
 251 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
 252             165                 170                 175
 254 caa tta gca gac cat tat caa caa aat act cca att ggc gat ggc cct      576
 255 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 256             180                 185                 190
 258 gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc ctt tcc      624
 259 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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262 aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta        672
263 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
264      210               215               220
266 aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa taa           717
267 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
268 225               230               235
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275 <211> LENGTH: 238
277 <212> TYPE: PRT
279 <213> ORGANISM: Aequorea victoria
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286 1                 5                 10                15
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290                20                25                30
293 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
294                35                40                45
297 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
298      50                55                60
301 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
302 65                70                75                80
305 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
306                85                90                95
309 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
310                100               105               110
313 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
314           115               120               125
317 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
318      130               135               140
321 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
322 145               150               155               160
325 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
326           165               170               175
329 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
330           180               185               190
333 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
334           195               200               205
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351 <213> ORGANISM: Aequorea victoria
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RAW SEQUENCE LISTING   DATE: 11/05/2001
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370 gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt gga gag      96
371 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
372             20                 25                 30
374 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc     144
375 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
376         35                 40                 45
378 act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc     192
379 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
380         50                 55                 60
382 tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag     240
383 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
384 65                 70                 75                 80
386 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga     288
387 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
388                 85                 90                 95
390 act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc     336
391 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
392             100                105                110
394 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att     384
395 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
396         115                120                125
398 gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat     432
399 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
400         130                135                140
402 tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc     480
403 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
404 145                150                155                160
406 atg gaa tac aat tat aac tca cat aat gta tac atc atg gca gac aaa     528
407 Met Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
408             165                170                175
410 cca aag aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa     576
411 Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys
412             180                185                190
414 gat gga agc gtt caa tta gca gac cat tat caa caa aat act cca att     624
415 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
416             195                200                205
418 ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa     672
419 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
420         210                215                220
422 tct gcc ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt     720
423 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu
424 225                230                235                240
426 ctt gag ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta     768
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VERIFICATION SUMMARY   DATE: 11/05/2001
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L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date